

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0256 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15
 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30
 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45
 Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60
 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80
 Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95
 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110
 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125
 Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140
 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160
 Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175
 Glu Asp Gln Thr Lys Xaa Val Leu Xaa Tyr Tyr Gln Lys Lys Gly Val
 180 185 190
 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205
 Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220
 Val Thr Pro
 225

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: 2122022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCANGCCA AAGCCCTGGT ACCCGCGCGG TGGGGCCTCA GTCTGCGGCC ATGGGGCGT	60
CCGCGCGGCT GCTGCGAGCG GTGATCATGG GGGCCCCGGG CTCGGGCAAG GGCACCGTGT	120
CGTCGCGCAT CACTACACAC TTTCGAGCTGA AGCACCTCTC CAGCGGGGAC CTGCTCCGGG	180

ACAAACATGCT	GCAGGGCACA	GAAATTGGCG	TGTTAGCCAA	GGCTTTCATT	GACCAAGGGA	240
AACTCATCCC	AGATGATGTC	ATGACTCGGC	TGGCCCTTCA	TGAGCTGAAA	AATCTCACCC	300
AGTATAGCTG	GCTGTTGGAT	GGTTTTCCAA	GGACACTTCC	ACAGGCAGAA	GCCCTAGATA	360
GAGCTTATCA	GATCGACACA	GTGATTAACC	TGAATGTGCC	CTTGAGGTC	ATTAAACAAC	420
GCCTTACTGC	TCGCTGGATT	CATCCCGCCA	GTGGCCGAGT	CTATAACATT	GAATTCAACC	480
CTCCCAAAAC	TGTGGGCATT	GATGACCTGA	CTGGGGAGCC	TCTCATTCAAG	CGTGAGGATG	540
ATAAAACCAGA	GACGGTTATC	AAGAGACTAA	AGGCTTATGA	AGACCAAACA	AAGNCAGTCC	600
TGGNATATTA	CCAGAAAAAA	GGGGTCTGG	AAACATTCTC	CGGAACAGAA	ACCAACAAGA	660
TTTGGCCCTA	TGTATATGCT	TTCTTACAAA	CTAAAGTTCC	ACAAAGAAGC	CAGAAAGCTT	720
CAGTTACTCC	ATGAGGAGAA	ATGTGTGTAA	CTATTAATAG	TAAGATGGGC	AAACCTCCTA	780
GTCTTGCAT	TTAGAAGCTG	CTTTCTAA	GACTTCTAGT	ATGTATGAAT	TCTTGAAAAA	840
TTATATTACT	TTTA					854

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 217576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Ala	Ser	Ala	Arg	Leu	Leu	Arg	Ala	Ala	Ile	Met	Gly	Ala	Pro
1		5			10							15			
Gly	Ser	Gly	Lys	Gly	Thr	Val	Ser	Ser	Arg	Ile	Thr	Lys	His	Phe	Glu
			20			25						30			
Leu	Lys	His	Leu	Ser	Ser	Gly	Asp	Leu	Leu	Arg	Asp	Asn	Met	Leu	Arg
	35					40						45			
Gly	Thr	Glu	Ile	Gly	Val	Leu	Ala	Lys	Thr	Phe	Ile	Asp	Gln	Gly	Lys
	50				55					60					
Leu	Ile	Pro	Asp	Asp	Val	Met	Thr	Arg	Leu	Val	Leu	His	Glu	Leu	Lys
	65				70				75			80			
Asn	Leu	Thr	Gln	Tyr	Asn	Trp	Leu	Leu	Asp	Gly	Phe	Pro	Arg	Thr	Leu
			85				90					95			
Pro	Gln	Ala	Glu	Ala	Leu	Asp	Arg	Ala	Tyr	Gln	Ile	Asp	Thr	Val	Ile
	100				105						110				
Asn	Leu	Asn	Val	Pro	Phe	Glu	Val	Ile	Lys	Gln	Arg	Leu	Thr	Ala	Arg
	115				120						125				
Trp	Ile	His	Pro	Gly	Ser	Gly	Arg	Val	Tyr	Asn	Ile	Glu	Phe	Asn	Pro
	130				135						140				
Pro	Lys	Thr	Met	Gly	Ile	Asp	Asp	Leu	Thr	Gly	Glu	Pro	Leu	Val	Gln
	145				150				155			160			
Arg	Glu	Asp	Asp	Arg	Pro	Glu	Thr	Val	Val	Lys	Arg	Leu	Lys	Ala	Tyr
					165			170			175				
Glu	Ala	Gln	Thr	Glu	Pro	Val	Leu	Glu	Tyr	Tyr	Arg	Lys	Lys	Gly	Val
	180					185					190				
Leu	Glu	Thr	Phe	Ser	Gly	Thr	Glu	Thr	Asn	Lys	Ile	Trp	Pro	His	Val
	195					200					205				
Tyr	Ala	Phe	Leu	Gln	Thr	Lys	Leu	Pro	Gln	Arg	Ser	Gln	Glu	Thr	Ser

210	215	220
Val Thr Pro		
225		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 450312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Ser Gly Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro	1	5
	10	15
Gly Ser Gly Lys Gly Thr Gly Ser Ser Arg Ile Thr Lys His Phe Glu	20	25
		30
Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Gln Asn Met Leu Gln	35	40
		45
Gly Thr Glu Ile Ala Val Leu Ala Lys Ser Phe Ile Asp Gln Gly Lys	50	55
		60
Leu Ile Pro Asp Asp Asp Met Thr Arg Leu Ala Leu His Glu Leu Lys	65	70
		75
		80
Asn Leu Thr Gln Cys Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu	85	90
		95
Pro Gln Ala Glu Ala Leu Asp Arg Val Tyr Gln Ile Asp Thr Val Ile	100	105
		110
Asn Leu Asn Val Pro Phe Glu Val Ile Lys Leu Arg Leu Thr Ala Arg	115	120
		125
Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro	130	135
		140
Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln	145	150
		155
		160
Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr	165	170
		175
Glu Ala Gln Thr Glu Pro Val Leu Gln Tyr Tyr Gln Lys Lys Gly Val	180	185
		190
Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Arg Pro His Val	195	200
		205
Tyr Ser Phe Leu Gln Met Lys Val Pro Glu Thr Ile Gln Lys Ala Ser	210	215
		220
Val Thr Pro		
225		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank
 (B) CLONE: 28577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ser Lys Leu Leu Arg Ala Val Ile Leu Gly Pro Pro Gly Ser
 1 5 10 15
 Gly Lys Gly Thr Val Cys Gln Arg Ile Ala Gln Asn Phe Gly Leu Gln
 20 25 30
 His Leu Ser Ser Gly His Phe Leu Arg Glu Asn Ile Lys Ala Ser Thr
 35 40 45
 Glu Val Gly Glu Met Ala Lys Gln Tyr Ile Glu Lys Ser Leu Leu Val
 50 55 60
 Pro Asp His Val Ile Thr Arg Leu Met Met Ser Glu Leu Glu Asn Arg
 65 70 75 80
 Arg Gly Gln His Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu Gly Gln
 85 90 95
 Ala Glu Ala Leu Asp Lys Ile Cys Glu Val Asp Leu Val Ile Ser Leu
 100 105 110
 Asn Ile Pro Phe Glu Thr Leu Lys Asp Arg Leu Ser Arg Arg Trp Ile
 115 120 125
 His Pro Pro Ser Gly Arg Val Tyr Asn Leu Asp Phe Asn Pro Pro His
 130 135 140
 Val His Gly Ile Asp Asp Val Thr Gly Glu Pro Leu Val Gln Gln Glu
 145 150 155 160
 Asp Asp Lys Pro Glu Ala Val Ala Ala Arg Leu Arg Gln Tyr Lys Asp
 165 170 175
 Val Ala Lys Pro Val Ile Glu Leu Tyr Lys Ser Arg Gly Val Leu His
 180 185 190
 Gln Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val Tyr Thr
 195 200 205
 Leu Phe Ser Asn Lys Ile Thr Pro Ile Gln Ser Lys Glu Ala Tyr
 210 215 220